



1/28

SEQUENCE LISTING

<110> Abbott Laboratories
Mukerji, Pradip
Huang, Yung-Sheng
Pereira, Suzette L.

<120> DESATURASE GENES, ENZYMES ENCODED
THEREBY, AND USES THEREOF

<130> 6884.US.01

<140> 10/060,793

<141> 2002-01-30

<160> 60

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward Primer R01144

<400> 1

atcgcgcgcgcg ccattcccaaa gcaactgctgg gtcaag

36

<210> 2

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward Primer R01119

<221> misc_feature

<222> (21)...(21)

<223> y = t/u or c at position 21

<221> misc_feature

<222> (33)...(33)

<223> y = t/u or c at position 33

<400> 2

gcctcttcg tctctggcca ygactgcggc cayggctcgt tctcg

45

<210> 3

<211> 45

<212> DNA

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<220>

<223> Reverse Primer R01118

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<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (30)...(31)
<223> r = g or a at positions 30-31

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (38)...(38)
<223> r = g or a at position 38

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43

<400> 3
gagrtggtar tgggggatct gggggaagar rtgrtggrg acrtg

<210> 4
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<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO1121

<221> misc_feature
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<223> y = t/u or c at position 9

<221> misc_feature
<222> (27)...(27)
<223> y = t/u or c at position 27

<221> misc_feature
<222> (36)...(36)
<223> y = t/u or c at position 36

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<400> 4

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ccctaccayg gctggcgcat ctcgcaycg acccaycayc agaac

45

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<220>
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<221> misc_feature
 <222> (7)...(7)
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<221> misc_feature
 <222> (10)...(10)
 <223> r = g or a at position 10

<221> misc_feature
 <222> (37)...(37)
 <223> r = g or a at position 37

<400> 5
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45

<210> 6
 <211> 36
 <212> DNA
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<220>
 <223> Forward Primer R01146

<221> misc_feature
 <222> (13)...(13)
 <223> s = g or c at position 13

<221> misc_feature
 <222> (19)...(19)
 <223> k = g or t/u at position 19

<400> 6
 ggctcgcaact tcsacccka ctcggacctc ttcgtc

36

<210> 7
 <211> 36
 <212> DNA
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<220>
 <223> Reverse Primer R01147

<221> misc_feature
 <222> (18)...(18)
 <223> m = a or c at position 18

<221> misc_feature

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<222> (24)...(24)
<223> w = a or t/u at position 24

<400> 7
gacgaagagg tccgagtmgg ggtwgaagtg cgagcc

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer R01148

<221> misc_feature
<222> (9)...(9)
<223> k = g or t/u at position 9

<221> misc_feature
<222> (30)...(30)
<223> w = a or t/u at position 30

<221> misc_feature
<222> (32)...(32)
<223> s = g or c at position 32

<400> 8
gcgctggakg gtggtgaggc cgccgaggaw gsacgacca

<210> 9
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer R01114

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (40)...(40)
<223> r = g or a at position 40

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43

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36

39

<400> 9
ctgggggaag agrtgrtgga tgacrtgggt gccgatgtor tgrtg

45

<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1116

<221> misc_feature
<222> (12)...(12)
<223> y = t/u or c at position 12

<221> misc_feature
<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (22)...(22)
<223> r = g or a at position 22

<221> misc_feature
<222> (33)...(33)
<223> k = g or t/u at position 33

<221> misc_feature
<222> (42)...(43)
<223> r = g or at at positions 42-43

<400> 10
ggtggcctcg ayyagrtggt artgggggat ctkggggaag arrtg

45

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO1118

<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (30)...(31)
<223> r = g or a at positions 30-31

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

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<221> misc_feature
<222> (38)...(38)
<223> r = g or a at position 38

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<221> misc_feature
<222> (43)...(43)
<223> r = g or a at position 43

<400> 11
gagrtggtar tgggggatct gggggaagar rtgrtggryg acrtg      45

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R01188

<400> 12
tacggtacc tcacgtactc gctcg      25

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R01189

<400> 13
ttcttgacc acaacgacga agcgacg      27

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R01190

<400> 14
ggagtggaag tacgtcaagg gcaac      25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R01191

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<400> 15 tcaaggga cctctcgagc gtcgac	26
<210> 16 <211> 31 <212> DNA <213> Artificial Sequence	
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<400> 16 cccagtcacg acgttgtaaa acgacggcca g	31
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<400> 17 agcggataac aatttcacac aggaacacgc	30
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<220> <223> Reverse Primer R01185	
<400> 18 ggtaaaagat ctcgctccttg tcgatgttgc	30
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<220> <223> Reverse Primer R01186	
<400> 19 gtcaaaagtgg ctcatcgtgc	20
<210> 20 <211> 26 <212> DNA <213> Artificial Sequence	
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<400> 20 cgagcgagta cgtgaggtac gcgtac	26

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<210> 21
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R01212

<400> 21
tcaacagaat tcatgaccga ggataagacg aaggtcgagt tcccg          45

<210> 22
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer R01213

<400> 22
aaaagaaagc ttcgcttcct agtcttagtc cgacttggcc ttggc          45

<210> 23
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R01221

<400> 23
tcaacaaagc ttatgaccga ggataagacg aaggtcgagt tcccg          45

<210> 24
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer R01222

<400> 24
aaaagagaat tccgcttcct agtcttagtc cgacttggcc ttggc          45

<210> 25
<211> 1077
<212> DNA
<213> Saprolegnia diclina

<400> 25
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ccgaacgcgt gctttgagtc gaacctcggc ctctcgctct actacaacggc ccgcgcgatc      120
ttcaacgcgt cggcctcggc ggcgtgctc tacgcggcgc gctcgaacgc gtccattggc      180
gataacgttc tgcctcaacg gctcgtttgc gccacctaca tctacgtgca gggcgctcgc      240
ttctggggct tcttcacggt cggccacgac tgcggccact cggccttctc gcgctaccac      300
agcgctcaact ttatcatcgg ctgcatcatg cactctgcga ttttgacgcc gtttcgagagc      360

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tggcgcggtga cgcaccgccca ccaccacaag aacacgggca acattgataa ggacgagatc 420
ttttaccgcg accggtcggt caaggacctc caggacgtgc gccaatgggt ctacacgctc 480
ggcggtgcgt ggtttgtcta ctggaaggtc gggatgccc cgcgacgat gagccattt 540
gaccgcgtggg acccgctcct ccttcgcgcg gcgtcggcg tcactggtgc gctcggcgtc 600
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<210> 26

<211> 358

<212> PRT

<213> Saprolegnia diclina

<400> 26

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Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
 20          25          30
Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
 35          40          45
Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
 50          55          60
Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
 65          70          75          80
Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
 85          90          95
Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
100          105          110
Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
115          120          125
His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
130          135          140
Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
145          150          155          160
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
165          170          175
Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
180          185          190
Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
195          200          205
Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
210          215          220
Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
225          230          235          240
Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
245          250          255
Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
260          265          270
Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
275          280          285
Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
290          295          300

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Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
 305 310 315 320
 Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
 325 330 335
 Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala
 340 345 350
 Ala Lys Ala Lys Ser Asp
 355

<210> 27
 <211> 1413
 <212> DNA
 <213> *Saprolegnia diclina*

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 gttggcgagt acttcaagaa gaacaacctc catccgcagg acggctctcc gggcctctgg 420
 cgcgatggg tcgtgtttgc ggtcgccggc ctgccttggt acggcatgca cttttcgact 480
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 ctccacgcca tgcacgactc gtcgcacgcg tcgtacacca acatgcgctt ctccattac 600
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 ccggcgatcg ccgccatcat cgtcgacgtc tgcaaggagt acaacatcaa gtacgccatc 1320
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 cagggcatcg ccgcacagat ccacatgggc taa 1413

<210> 28
 <211> 819
 <212> DNA
 <213> *Thraustochytrid* sp.

<400> 28
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 accatgctgg cattcgaggt gggatacatg gccatgctgc tcttcggcat cccgatcatg 180
 aagcagatgg agaagccttt tgagctcaag accatcaagc tcttgacaaa cttgtttctc 240
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 aaagtgtttg gaaacgacat gaggaaagggc aacgagtctc atgtcgaggc catgtctcgc 360
 atcgtgtacg ttgtctcgct gtccaaggca tacgagttct tggataccgc catcatgac 420
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 gggttcgtga agccaatcaa gccgtacatc accacccttc agatgaccca gttcatggca 660

atgcttgtgc agtccttgtga cgactacctc ttcccatgcg actaccacaca ggctcttgtg	720
cagcttcttg gagggtacat gatcaccttg ctggccctct tcggcaactt ttttgtgcag	780
agctatctta aaaagccaaa aaagagcaag accaactaa	819

<210> 29

<211> 515

<212> PRT

<213> Saprolegnia diclina

<400> 29

Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn	
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20 25 30	
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35 40 45	
Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile	
50 55 60	
Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu	
65 70 75 80	
Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp	
85 90 95	
Ser Ala Ser Tyr Trp Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg	
100 105 110	
Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala	
115 120 125	
Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp	
130 135 140	
Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met	
145 150 155 160	
Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys	
165 170 175	
Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met	
180 185 190	
Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met	
195 200 205	
Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu	
210 215 220	
Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp	
225 230 235 240	
Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr	
245 250 255	
Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys	
260 265 270	
Phe Gln His Leu Tyr Ala Pro Leu Ile Phe Gly Phe Met Thr Ile Asn	
275 280 285	
Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe	
290 295 300	
Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Asn Val Ala Arg	
305 310 315 320	
Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro	
325 330 335	
Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala	
340 345 350	
His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His	
355 360 365	
Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val	

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      370              375              380
Met Ala Pro Pro Arg Thr Val His Gly Val Thr Pro Met Gln Val Thr
385              390              395              400
Gln Lys Ala Leu Ser Ala Ala Glu Ser Thr Lys Ser Asp Ala Asp Lys
      405              410              415
Thr Thr Met Ile Pro Leu Asn Asp Trp Ala Ala Val Gln Cys Gln Thr
      420              425              430
Ser Val Asn Trp Ala Val Gly Ser Trp Phe Trp Asn His Phe Ser Gly
      435              440              445
Gly Leu Asn His Gln Ile Glu His His Cys Phe Pro Gln Asn Pro His
      450              455              460
Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu
465              470              475              480
Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe
      485              490              495
Lys Met Leu Ser His Leu Arg Thr Leu Gly Asn Glu Asp Leu Thr Ala
      500              505              510
Trp Ser Thr
      515

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<210> 30
<211> 51
<212> DNA
<213> Artificial Sequence

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<220>
<223> Forward Primer R0967

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<221> misc_feature
<222> (4)...(4)
<223> s = g or c at position 4

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<221> misc_feature
<222> (12)...(12)
<223> s = g or c at position 12

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<221> misc_feature
<222> (30)...(30)
<223> s = g or c at position 30

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<221> misc_feature
<222> (31)...(31)
<223> k = g or t/u at position 31

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<221> misc_feature
<222> (32)...(32)
<223> s = g or c at position 32

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<400> 30
ccgsagttca csatcaagga gatccgcgag kscatcccg cccactgtct c

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51

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<210> 31
<211> 48
<212> DNA
<213> Artificial Sequence
<220>

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<223> Reverse Primer R0968

<221> misc_feature

<222> (2)...(2)

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<221> misc_feature

<222> (3)...(3)

<223> s = g or c at position 3

<221> misc_feature

<222> (12)...(12)

<223> k = g or t/u at position 12

<221> misc_feature

<222> (17)...(17)

<223> w = a or t/u at position 17

<221> misc_feature

<222> (18)...(18)

<223> m = a or c at position 18

<221> misc_feature

<222> (19)...(19)

<223> s = g or c at position 19

<221> misc_feature

<222> (41)...(41)

<223> w = a or t/u at position 41

<221> misc_feature

<222> (42)...(42)

<223> r = g or a at position 42

<400> 31

grscttcttg akgtggwmsg tggcctcctc ggcgtggtag wrccgcat

48

<210> 32

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward Primer R0964

<221> misc_feature

<222> (3)...(4)

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<221> misc_feature

<222> (25)...(25)

<223> r = g or a at position 25

<221> misc_feature

<222> (36)...(36)

<223> s = g or c at position 36

<400> 32
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45

<210> 33
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R0965

<221> misc_feature
<222> (3)...(4)
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<221> misc_feature
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<221> misc_feature
<222> (17)...(17)
<223> y = t/u or c at position 17

<221> misc_feature
<222> (18)...(18)
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<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (31)...(31)
<223> k = g or t/u at position 31

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<221> misc_feature
<222> (36)...(36)
<223> s = g or c at position 36

<400> 33
ccsstctact ggatcrysca gggtrtcgct kgyacsggtg tctgg

45

<210> 34
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer R0966

<221> misc_feature
<222> (19)...(19)
<223> s = g or c at position 19

```

<221> misc_feature
<222> (20)...(21)
<223> m = a or c at positions 20-21

<221> misc_feature
<222> (30)...(30)
<223> r = g or a at position 30

<400> 34
ggcgtggtag tgcggcatcm mcgagaagar gtgggtgggcg acgtg
45

<210> 35
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R0975

<400> 35
cacgtacctc cagcacacgg acacctacg
29

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer R0976

<400> 36
gatcgacagc gcgatccacc acattgc
27

<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer R0977

<400> 37
caaatggtaa aagctagtg ggcgcgtgc
29

<210> 38
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer R0978

<400> 38
agtagctgcc ctggacgaac cagtagatg
29

<210> 39

```

<211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward Primer R01051

<400> 39
 tcaacagaat tcatgtgcaa aggtcaagct ccttccaagg ccgacgtg 48

<210> 40
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse Primer R01057

<400> 40
 aaaagaaagc ttttactttt cctcgagctt gcgcttgtaa aacacaaac 48

<210> 41
 <211> 1182
 <212> DNA
 <213> *Saprolegnia diclina*

<400> 41
 atgtgcaaaag gtcaagctcc ttccaaggcc gacgtgttcc acgctgcggg gtaccgcccg 60
 gtcgcccggca cgcccagacc gctgcccgtg gagccccga cgatcacgct caaggacctg 120
 cgcgcgggca tcccggccca ctgctttgag cgcacgcgtg ccactagctt ttaccatttg 180
 gccaaagaac ttgcgatctg cgcgcggcgtg ttgcgcgttg gcctcaagct cgcggctgcc 240
 gacttgccgc tcgcggccaa gctggctcgc tggcccatct actggttcgt ccagggcacg 300
 tactttacgg gcatctgggt cattgcgcac gaatcgcggc accaggcgtt ctgcgcgtcc 360
 gagatcctca acgacacggt cgggtatcatt ctctactcgc tctcttttgt gccgtaccac 420
 agctggaaga tcacgcaccg ccgcaccacc tccaacacgg gcagctgcga gaacgacgag 480
 gtgtttaacg cgacgcggcg gtccgtcgtc gaggccaaag acgaccactc gctcctcgaa 540
 gagagccccg tctacaacct gtacggcacc gtcgatgatg ttctcgtggg ctggatgccg 600
 ggctacctct tcttcaacgc gaccggcccg accaagtacg ctggcctcgc caagtgcgac 660
 ttcaaccggt acgcagcctt ttctctccca aaggagcgcc tcagcatctg gtggagcgac 720
 ctctgcttcc tcgcggcctt gtacggcttt ggctacggcg tctcggtctt cggcctctct 780
 gatgtcgccc gccactacat cgtgccgtac ctcatattga acgcgtacct cgtgctcact 840
 acgtacctcc agcacacgga tacgtacgtg cccacttcc gcggcgacga gtggaactgg 900
 ctgcgcggcg cgctctgcac cgtcgaccgc tcgttcggcg cgtggatcga cagcgcgac 960
 caccacattg ccgacacgca cgtgacgcac cacattttct ccaagacgcc ctctaccac 1020
 gcgatcgagg cgaccgacgc catcacgccc ctccctcggc agtactacct catcgaccg 1080
 acgcgatccc cgtggcgctt ctggcgctcg ttacgcact gcaagtacgt cgaggacgac 1140
 ggcaacgctg tgttttcaaa gcgcaagctc gaggaaaagt aa 1182

<210> 42
 <211> 393
 <212> PRT
 <213> *Saprolegnia diclina*

<400> 42
 Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
 1 5 10 15
 Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro


```

      20      25      30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
      35      40      45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
      50      55      60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
65      70      75      80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
      85      90      95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
      100      105      110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
      115      120      125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
      130      135      140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145      150      155      160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
      165      170      175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
      180      185      190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
      195      200      205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
210      215      220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225      230      235      240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
      245      250      255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
      260      265      270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
      275      280      285
Tyr Val Pro His Phe Arg Gly Asp Glu Trp Asn Trp Leu Arg Gly Ala
290      295      300
Leu Cys Thr Val Asp Arg Ser Phe Gly Ala Trp Ile Asp Ser Ala Ile
305      310      315      320
His His Ile Ala Asp Thr His Val Thr His His Ile Phe Ser Lys Thr
      325      330      335
Pro Phe Tyr His Ala Ile Glu Ala Thr Asp Ala Ile Thr Pro Leu Leu
340      345      350
Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro Leu Ala Leu Trp
355      360      365
Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp Gly Asn Val Val
370      375      380
Phe Tyr Lys Arg Lys Leu Glu Glu Lys
385      390

```

<210> 43

<211> 393

<212> PRT

<213> *Saprolegnia diclina*

<400> 43

```

Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
  1      5      10      15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro

```

Pro	Thr	Ile	Thr	Leu	Lys	Asp	Leu	Arg	Ala	Ala	Ile	Pro	Ala	His	Cys
		35					40					45			
Phe	Glu	Arg	Ser	Ala	Ala	Thr	Ser	Phe	Tyr	His	Leu	Ala	Lys	Asn	Leu
	50						55				60				
Ala	Ile	Cys	Ala	Gly	Val	Phe	Ala	Val	Gly	Leu	Lys	Leu	Ala	Ala	Ala
65					70					75					80
Asp	Leu	Pro	Leu	Ala	Ala	Lys	Leu	Val	Ala	Trp	Pro	Ile	Tyr	Trp	Phe
				85					90					95	
Val	Gln	Gly	Thr	Tyr	Phe	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys
			100					105					110		
Gly	His	Gln	Ala	Phe	Ser	Ala	Ser	Glu	Ile	Leu	Asn	Asp	Thr	Val	Gly
		115					120					125			
Ile	Ile	Leu	His	Ser	Leu	Leu	Phe	Val	Pro	Tyr	His	Ser	Trp	Lys	Ile
	130					135					140				
Thr	His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser	Cys	Glu	Asn	Asp	Glu
145					150					155					160
Val	Phe	Thr	Pro	Thr	Pro	Arg	Ser	Val	Val	Glu	Ala	Lys	His	Asp	His
					165				170					175	
Ser	Leu	Leu	Glu	Glu	Ser	Pro	Leu	Tyr	Asn	Leu	Tyr	Gly	Ile	Val	Met
			180					185					190		
Met	Leu	Leu	Val	Gly	Trp	Met	Pro	Gly	Tyr	Leu	Phe	Phe	Asn	Ala	Thr
		195					200					205			
Gly	Pro	Thr	Lys	Tyr	Ala	Gly	Leu	Ala	Lys	Ser	His	Phe	Asn	Pro	Tyr
	210					215					220				
Ala	Ala	Phe	Phe	Leu	Pro	Lys	Glu	Arg	Leu	Ser	Ile	Trp	Trp	Ser	Asp
225					230					235					240
Leu	Cys	Phe	Leu	Ala	Ala	Leu	Tyr	Gly	Phe	Gly	Tyr	Gly	Val	Ser	Val
				245						250				255	
Phe	Gly	Leu	Leu	Asp	Val	Ala	Arg	His	Tyr	Ile	Val	Pro	Tyr	Leu	Ile
			260					265					270		
Cys	Asn	Ala	Tyr	Leu	Val	Leu	Ile	Thr	Tyr	Leu	Gln	His	Thr	Asp	Thr
	275						280					285			
Tyr	Val	Pro	His	Phe	Arg	Gly	Asp	Glu	Trp	Asn	Trp	Leu	Arg	Gly	Ala
290						295				300					
Leu	Cys	Thr	Val	Asp	Arg	Ser	Phe	Gly	Ala	Trp	Ile	Asp	Ser	Ala	Ile
305					310				315						320
His	His	Ile	Ala	Asp	Thr	His	Val	Thr	His	His	Ile	Phe	Ser	Lys	Thr
				325					330					335	
Pro	Phe	Tyr	His	Ala	Ile	Glu	Ala	Thr	Asp	Ala	Ile	Thr	Pro	Leu	Leu
			340					345					350		
Gly	Lys	Tyr	Tyr	Leu	Ile	Asp	Pro	Thr	Pro	Ile	Pro	Leu	Ala	Leu	Trp
		355					360					365			
Arg	Ser	Phe	Thr	His	Cys	Lys	Tyr	Val	Glu	Asp	Asp	Gly	Asn	Val	Val
	370					375					380				
Phe	Tyr	Lys	Arg	Lys	Leu	Glu	Glu	Lys							
385					390										

<210> 44

<211> 359

<212> PRT

<213> Synechocystis sp.

<220>

<221> VARIANT

<222> (315)...(315)

<223> Xaa = Unknown or Other at position 315

<221> VARIANT
 <222> (331)...(331)
 <223> Xaa = Unknown or Other at position 331

<400> 44

```

Tyr Phe Phe Leu Asp Val Gly Leu Ile Ala Gly Phe Tyr Ala Leu Ala
  1           5           10           15
Ala Tyr Leu Asp Ser Trp Phe Phe Tyr Pro Ile Phe Trp Leu Ile Gln
  20           25           30
Gly Thr Leu Phe Trp Ser Leu Phe Val Val Gly His Asp Cys Gly His
  35           40           45
Gly Ser Phe Ser Lys Ser Lys Thr Leu Asn Asn Trp Ile Gly His Leu
  50           55           60
Ser His Thr Pro Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His
  65           70           75
Arg Thr His His Ala Asn Thr Gly Asn Ile Asp Thr Asp Glu Ser Trp
  85           90           95
Tyr Pro Val Ser Glu Gln Lys Tyr Asn Gln Met Ala Trp Tyr Glu Lys
  100          105          110
Leu Leu Arg Phe Tyr Leu Pro Leu Ile Ala Tyr Pro Ile Tyr Leu Phe
  115          120          125
Arg Arg Ser Pro Asn Arg Gln Gly Ser His Phe Met Pro Gly Ser Pro
  130          135          140
Leu Phe Arg Pro Gly Glu Lys Ala Ala Val Leu Thr Ser Thr Phe Ala
  145          150          155
Leu Ala Ala Phe Val Gly Phe Leu Gly Phe Leu Thr Trp Gln Phe Gly
  165          170          175
Trp Leu Phe Leu Leu Lys Phe Tyr Val Ala Pro Tyr Leu Val Phe Val
  180          185          190
Val Trp Leu Asp Leu Val Thr Phe Leu His His Thr Glu Asp Asn Ile
  195          200          205
Pro Trp Tyr Arg Gly Asp Asp Trp Tyr Phe Leu Lys Gly Ala Leu Ser
  210          215          220
Thr Ile Asp Arg Asp Tyr Gly Phe Ile Asn Pro Ile His His Asp Ile
  225          230          235
Gly Thr His Val Ala His His Ile Phe Ser Asn Met Pro His Tyr Lys
  245          250          255
Leu Arg Arg Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr
  260          265          270
Arg Tyr Ser Asp Glu Pro Ile Trp Gln Ala Phe Phe Lys Ser Tyr Trp
  275          280          285
Ala Cys His Phe Val Pro Asn Gln Gly Ser Gly Val Tyr Tyr Gln Ser
  290          295          300
Pro Ser Asn Gly Gly Tyr Gln Lys Lys Pro Xaa Leu Ile Leu Ile Glu
  305          310          315
Ser Asn Gln His Arg Glu Gly Arg Gln Tyr Xaa Met Val Leu Leu Pro
  325          330          335
Ser Asp Arg Leu Met Arg Ser Met Glu Glu Val Lys Gln Ser His Ser
  340          345          350
Lys Arg Ser Ala Leu Asn Gln
  355

```

<210> 45
 <211> 358
 <212> PRT
 <213> Saprolegnia diclina

<400> 45
 Met Thr Glu Asp Lys Thr Lys Val Glu Phe Pro Thr Leu Thr Glu Leu
 1 5 10 15
 Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
 20 25 30
 Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
 35 40 45
 Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
 50 55 60
 Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
 65 70 75 80
 Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
 85 90 95
 Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
 100 105 110
 Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
 115 120 125
 His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
 130 135 140
 Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
 145 150 155 160
 Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
 165 170 175
 Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Arg Arg Ala Ser
 180 185 190
 Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
 195 200 205
 Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
 210 215 220
 Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
 225 230 235 240
 Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
 245 250 255
 Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
 260 265 270
 Phe Val Asp Asn Leu Ser His Ile Gly Thr His Gln Val His His
 275 280 285
 Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
 290 295 300
 Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
 305 310 315 320
 Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
 325 330 335
 Val Pro Glu Thr Ala Gln Ile Phe Thr Lys Leu Lys Glu Ser Ala Ala Ala
 340 345 350
 Ala Lys Ala Lys Ser Asp
 355

<210> 46
 <211> 409
 <212> PRT
 <213> *Caenorhabditis elegans*

<220>
 <221> VARIANT
 <222> (389)...(389)

<223> Xaa = Unknown or Other at position 389

<400> 46

```

Val Thr Gly Gly Asp Val Leu Val Asp Ala Arg Ala Ser Leu Glu Glu
 1          5          10          15
Lys Glu Ala Pro Arg Asp Val Asn Ala Asn Thr Lys Gln Ala Thr Thr
      20          25          30
Glu Glu Pro Arg Ile Gln Leu Pro Thr Val Asp Ala Phe Arg Arg Ala
      35          40          45
Ile Pro Ala His Cys Phe Glu Arg Asp Leu Val Lys Ser Ile Arg Tyr
      50          55          60
Leu Val Gln Asp Phe Ala Ala Leu Thr Ile Leu Tyr Phe Ala Leu Pro
      65          70          75          80
Ala Phe Glu Tyr Phe Gly Leu Phe Gly Tyr Leu Val Trp Asn Ile Phe
      85          90          95
Met Gly Val Phe Gly Phe Ala Leu Phe Val Val Gly His Asp Cys Leu
      100          105          110
His Gly Ser Phe Ser Asp Asn Gln Asn Leu Asn Asp Phe Ile Gly His
      115          120          125
Ile Ala Phe Ser Pro Leu Phe Ser Pro Tyr Phe Pro Trp Gln Lys Ser
      130          135          140
His Lys Leu His His Ala Phe Thr Asn His Ile Asp Lys Asp His Gly
      145          150          155          160
His Val Trp Ile Gln Asp Lys Asp Trp Glu Ala Met Pro Ser Trp Lys
      165          170          175
Arg Trp Phe Asn Pro Ile Pro Phe Ser Gly Trp Leu Lys Trp Phe Pro
      180          185          190
Val Tyr Thr Leu Phe Gly Phe Cys Asp Gly Ser His Phe Trp Pro Tyr
      195          200          205
Ser Ser Leu Phe Val Arg Asn Ser Asp Arg Val Gln Cys Val Ile Ser
      210          215          220
Gly Ile Cys Cys Cys Val Cys Ala Tyr Ile Ala Leu Thr Ile Ala Gly
      225          230          235          240
Ser Tyr Ser Asn Trp Phe Trp Tyr Tyr Trp Val Pro Leu Ser Phe Phe
      245          250          255
Gly Leu Met Leu Val Ile Val Thr Tyr Leu Gln His Val Asp Asp Val
      260          265          270
Ala Glu Val Tyr Glu Ala Asp Glu Trp Ser Phe Val Arg Gly Gln Thr
      275          280          285
Gln Thr Ile Asp Arg Tyr Tyr Gly Leu Gly Leu Asp Thr Thr Met His
      290          295          300
His Ile Thr Asp Gly His Val Ala His His Phe Phe Asn Lys Ile Pro
      305          310          315          320
His Tyr His Leu Ile Glu Ala Thr Glu Gly Val Lys Lys Val Leu Glu
      325          330          335
Pro Leu Ser Asp Thr Gln Tyr Gly Tyr Lys Ser Gln Val Asn Tyr Asp
      340          345          350
Phe Phe Ala Arg Phe Leu Trp Phe Asn Tyr Lys Leu Asp Tyr Leu Val
      355          360          365
His Lys Thr Ala Gly Ile Met Gln Phe Arg Thr Thr Leu Glu Glu Lys
      370          375          380
Ala Lys Ala Lys Xaa Lys Asn Ile Pro Cys Arg Ser Arg Val Gln Gln
      385          390          395          400
Gln Leu Leu Arg Phe His Arg Phe Cys
      405

```

<210> 47

<211> 333
 <212> PRT
 <213> *Saprolegnia diclina*

<400> 47

```

Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
 1          5          10          15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Glu Pro
 20          25          30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
 35          40          45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
 50          55          60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
 65          70          75          80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
 85          90          95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
100          105          110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
115          120          125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
130          135          140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145          150          155          160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
165          170          175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
180          185          190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
195          200          205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
210          215          220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225          230          235          240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
245          250          255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
260          265          270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
275          280          285
Thr Pro Leu Leu Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro
290          295          300
Leu Ala Leu Trp Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp
305          310          315          320
Gly Asn Val Val Phe Tyr Lys Arg Lys Leu Glu Glu Lys
325          330

```

<210> 48
 <211> 412
 <212> PRT
 <213> *Gossypium hirsutum*

<220>

<221> VARIANT

<222> (9)...(9)

<223> Xaa = Unknown or Other at position 9

<221> VARIANT

<222> (403)...(403)

<223> Xaa = Unknown or Other at position 403

<400> 48

```

Leu Arg Val Ser Ser Thr Trp Arg Xaa Thr Ala Phe Phe Lys Ala Ser
 1          5          10          15
Lys Met Gly Ala Gly Arg Met Pro Ile Asp Gly Ile Lys Glu Glu
 20          25          30
Asn Arg Gly Ser Val Asn Arg Val Pro Ile Glu Lys Pro Phe Thr
 35          40          45
Leu Gly Gln Ile Lys Gln Ala Ile Pro Pro His Cys Phe Arg Arg Ser
 50          55          60
Leu Leu Arg Ser Phe Ser Tyr Val Val His Asp Leu Cys Leu Ala Ser
 65          70          75          80
Phe Phe Tyr Tyr Ile Ala Thr Ser Tyr Phe His Phe Leu Pro Gln Pro
 85          90          95
Phe Ser Tyr Ile Ala Trp Pro Val Tyr Trp Val Leu Gln Gly Cys Ile
100          105          110
Leu Thr Gly Val Trp Val Ile Ala His Glu Trp Gly His His Ala Phe
115          120          125
Arg Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu Ile Leu His Ser
130          135          140
Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His
145          150          155          160
His Ser Asn Thr Gly Ser Met Glu Arg Asp Glu Val Phe Val Pro Lys
165          170          175
Pro Lys Ser Lys Leu Ser Cys Phe Ala Lys Tyr Leu Asn Asn Pro Pro
180          185          190
Gly Arg Val Leu Ser Leu Val Val Thr Leu Thr Leu Gly Trp Pro Met
195          200          205
Tyr Leu Ala Phe Asn Val Ser Gly Arg Tyr Tyr Asp Arg Leu Ala Ser
210          215          220
His Tyr Asn Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
225          230          235          240
Val Tyr Ile Ser Asp Thr Gly Ile Phe Ala Val Ile Tyr Val Leu Tyr
245          250          255
Lys Ile Ala Ala Thr Lys Gly Leu Ala Trp Leu Leu Cys Thr Tyr Gly
260          265          270
Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
275          280          285
Gln His Thr His Ser Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
290          295          300
Trp Leu Arg Gly Ala Leu Ser Thr Met Asp Arg Asp Phe Gly Val Leu
305          310          315          320
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
325          330          335
Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
340          345          350
Lys Pro Ile Leu Gly Lys Tyr Tyr Pro Phe Asp Gly Thr Pro Ile Tyr
355          360          365
Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp
370          375          380
Val Gly Gly Gly Gly Gly Ser Lys Gly Val Phe Trp Tyr Arg Asn
385          390          395          400
Lys Phe Xaa Arg Pro Thr Asn Cys Leu Ile Ala Gly

```

405

410

<210> 49
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein Motif 1 from Example 3

<400> 49
 Thr Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys
 1 5 10

<210> 50
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein Motif 2 from Example 3

<400> 50
 Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
 1 5 10 15

<210> 51
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein Motif 3 from Example 3

<400> 51
 Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn
 1 5 10 15

<210> 52
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein Motif 4 from Example 3

<221> VARIANT
 <222> (5)...(5)
 <223> Xaa = D or H at position 5

<221> VARIANT
 <222> (7)...(7)
 <223> Xaa = D or Y at position 7

<400> 52
 Gly Ser His Phe Xaa Pro Xaa Ser Asp Leu Phe Val
 1 5 10

<210> 53
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein Motif 5 from Example 3

<221> VARIANT
 <222> (3)...(3)
 <223> Xaa = Y or F at position 3

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa = L or V at position 4

<221> VARIANT
 <222> (11)...(11)
 <223> Xaa = L or I at position 11

<400> 53
 Trp Ser Xaa Xaa Arg Gly Gly Leu Thr Thr Xaa Asp Arg
 1 5 10

<210> 54
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein Motif 6 from Example 3

<400> 54
 His His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln
 1 5 10 15

<210> 55
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein Motif 7 from Example 3

<221> VARIANT
 <222> (2)...(2)
 <223> Xaa = L or F at position 2

<221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Q or K at position 5

<221> VARIANT
 <222> (12)...(12)
 <223> Xaa = V or I at position 12

```

<400> 55
His Xaa Phe Pro Xaa Ile Pro His Tyr His Leu Xaa Glu Ala Thr
 1             5             10             15

<210> 56
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 8 from Example 3

<221> VARIANT
<222> (3)...(3)
<223> Xaa = A or I at position 3

<221> VARIANT
<222> (6)...(6)
<223> Xaa = L or F at position 6

<400> 56
His Val Xaa His His Xaa Phe Pro Gln Ile Pro His Tyr His Leu
 1             5             10             15

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 1 from Example 7

<221> VARIANT
<222> (2)...(2)
<223> Xaa = N or E at position 2

<221> VARIANT
<222> (10)...(10)
<223> Xaa = D or E at position 10

<221> VARIANT
<222> (11)...(11)
<223> Xaa = A or C at position 11

<400> 57
Pro Xaa Phe Thr Ile Lys Glu Ile Arg Xaa Xaa Ile Pro Ala His Cys
 1             5             10             15
Phe

<210> 58
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 2 from Example 7

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<221> VARIANT
<222> (3)...(3)
<223> Xaa = H or F at position 3

<221> VARIANT
<222> (11)...(11)
<223> Xaa = V or Y at position 11

<221> VARIANT
<222> (13)...(13)
<223> Xaa = I or L at position 13

<221> VARIANT
<222> (16)...(16)
<223> Xaa = A or L at position 16

<400> 58
Met Pro Xaa Tyr His Ala Glu Glu Ala Thr Xaa His Xaa Lys Lys Xaa
 1           5           10          15

<210> 59
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein Motif 3 from Example 7

<221> VARIANT
<222> (2)...(2)
<223> Xaa = L or V at position 2

<221> VARIANT
<222> (5)...(5)
<223> Xaa = A or I at position 5

<221> VARIANT
<222> (6)...(6)
<223> Xaa = C or M or A at position 6

<221> VARIANT
<222> (9)...(9)
<223> Xaa = V or I at position 9

<221> VARIANT
<222> (11)...(11)
<223> Xaa = L or G or C at position 11

<400> 59
Pro Xaa Tyr Trp Xaa Xaa Gln Gly Xaa Val Xaa Thr Gly Val Trp
 1           5           10          15

<210> 60
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>

<223> Protein Motif 4 from Example 7

<221> VARIANT

<222> (6)...(6)

<223> Xaa = L or F at position 6

<221> VARIANT

<222> (9)...(9)

<223> Xaa = T or Q at position 9 .

<400> 60

His	Val	Ala	His	His	Xaa	Phe	Ser	Xaa	Met	Pro	His	Tyr	His	Ala
1				5					10					15